



RECEIVED
APR 15 2002
TECH CENTER 1600/2900

SEQUENCE LISTING

<110> KOJIMA, Yoshinao
FUKUMOTO, Satoshi
FURUKAWA, Keiko
OKAJIMA, Tetsuya
FURUKAWA, Koichi

<120> ALPHA 1,4-GALACTOSYLTRANSFERASE AND DNA ENCODING THEREOF

<130> 195870US0

<140> 09/641,701

<141> 2000-08-21

<150> JP 2000-35454

<151> 2000-02-14

<160> 2

<170> PatentIn version 3.1

<210> 1

<211> 1975

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (134)..(1192)

<223>

<400> 1

aaggtcggct gctgagccag ggcgtgtctc ccggaggcct gtgggctgcc aggatcccca 60

cctctctgca atgggctgcc caggetgacc agccgggttc tgctggaagc tcttggtctg 120

atctggggat acc atg tcc aag ccc ccc gac ctc ctg ctg cgg ctg ctc 169
Met Ser Lys Pro Pro Asp Leu Leu Leu Arg Leu Leu
1 5 10

cgg ggc gcc cca agg cag cgg gtc tgc acc ctg ttc atc atc ggc ttc 217
Arg Gly Ala Pro Arg Gln Arg Val Cys Thr Leu Phe Ile Ile Gly Phe
15 20 25

aag ttc acg ttt ttc gtc tcc atc atg atc tac tgg cac gtt gtg gga 265
Lys Phe Thr Phe Phe Val Ser Ile Met Ile Tyr Trp His Val Val Gly
30 35 40

gag ccc aag gag aaa ggg cag ctc tat aac ctg cca gca gag atc ccc 313
Glu Pro Lys Glu Lys Gly Gln Leu Tyr Asn Leu Pro Ala Glu Ile Pro
45 50 55 60

tgc ccc acc ttg aca ccc ccc acc cca ccc tcc cac ggc ccc act cca 361
Cys Pro Thr Leu Thr Pro Pro Thr Pro Pro Ser His Gly Pro Thr Pro
65 70 75

ggc aac atc ttc ttc ctg gag act tca gac cgg acc aac ccc aac ttc 409
 Gly Asn Ile Phe Phe Leu Glu Thr Ser Asp Arg Thr Asn Pro Asn Phe
 80 85 90

ctg ttc atg tgc tgc gtg gag tgc gcc gcc aga act cac ccc gaa tcc 457
 Leu Phe Met Cys Ser Val Glu Ser Ala Ala Arg Thr His Pro Glu Ser
 95 100 105

cac gtg ctg gtc ctg atg aaa ggg ctt ccg ggt ggc aac gcc tct ctg 505
 His Val Leu Val Leu Met Lys Gly Leu Pro Gly Gly Asn Ala Ser Leu
 110 115 120

ccc cgg cac ctg ggc atc tca ctt ctg agc tgc ttc ccg aat gtc cag 553
 Pro Arg His Leu Gly Ile Ser Leu Leu Ser Cys Phe Pro Asn Val Gln
 125 130 135 140

atg ctc ccg ctg gac ctg cgg gag ctg ttc cgg gac aca ccc ctg gcc 601
 Met Leu Pro Leu Asp Leu Arg Glu Leu Phe Arg Asp Thr Pro Leu Ala
 145 150 155

gac tgg tac gcg gcc gtg cag ggg cgc tgg gag ccc tac ctg ctg ccc 649
 Asp Trp Tyr Ala Ala Val Gln Gly Arg Trp Glu Pro Tyr Leu Leu Pro
 160 165 170

gtg ctc tcc gac gcc tcc agg atc gca ctc atg tgg aag ttc ggc ggc 697
 Val Leu Ser Asp Ala Ser Arg Ile Ala Leu Met Trp Lys Phe Gly Gly
 175 180 185

atc tac ctg gac acg gac ttc att gtt ctc aag aac ctg cgg aac ctg 745
 Ile Tyr Leu Asp Thr Asp Phe Ile Val Leu Lys Asn Leu Arg Asn Leu
 190 195 200

acc aac gtg ctg ggc acc cag tcc cgc tac gtc ctc aac ggc gcg ttc 793
 Thr Asn Val Leu Gly Thr Gln Ser Arg Tyr Val Leu Asn Gly Ala Phe
 205 210 215 220

ctg gcc ttc gag cgc cgg cac gag ttc atg gcg ctg tgc atg cgg gac 841
 Leu Ala Phe Glu Arg Arg His Glu Phe Met Ala Leu Cys Met Arg Asp
 225 230 235

ttc gtg gac cac tac aac ggc tgg atc tgg ggt cac cag ggc ccg cag 889
 Phe Val Asp His Tyr Asn Gly Trp Ile Trp Gly His Gln Gly Pro Gln
 240 245 250

ctg ctc acg cgg gtc ttc aag aag tgg tgt tcc atc cgc agc ctg gcc 937
 Leu Leu Thr Arg Val Phe Lys Lys Trp Cys Ser Ile Arg Ser Leu Ala
 255 260 265

gag agc cgc gcc tgc cgc ggc gtc acc acc ctg ccc cct gag gcc ttc 985
 Glu Ser Arg Ala Cys Arg Gly Val Thr Thr Leu Pro Pro Glu Ala Phe
 270 275 280

tac ccc atc ccc tgg cag gac tgg aag aag tac ttt gag gac atc aac 1033
 Tyr Pro Ile Pro Trp Gln Asp Trp Lys Lys Tyr Phe Glu Asp Ile Asn
 285 290 295 300

ccg gag gag ctg ccg cgg ctg ctc agt gcc acc tat gct gtc cac gtg 1081
Pro Glu Glu Leu Pro Arg Leu Leu Ser Ala Thr Tyr Ala Val His Val
305 310 315

tgg aac aag aag agc cag ggc acg cgg ttc gag gcc acg tcc agg gca 1129
Trp Asn Lys Lys Ser Gln Gly Thr Arg Phe Glu Ala Thr Ser Arg Ala
320 325 330

ctg ctg gcc cag ctg cat gcc cgc tac tgc ccc acg acg cac gag gcc 1177
Leu Leu Ala Gln Leu His Ala Arg Tyr Cys Pro Thr Thr His Glu Ala
335 340 345

atg aaa atg tac ttg tgaggggccc gccagggtcac ctccccaacc tgctcctgat 1232
Met Lys Met Tyr Leu
350

ggggcactgg gccgcccttc ccggggaggc aagattgagg gcccgggaga gggaggcccg 1292

agctgccacc gggcttaggc aggtgttga ggagctgtgg gagcaggccc agtgggaggc 1352

tgtggacacc ccgaggacag tgtcctgtct cgaggcaggg ctgacacatg gtgccatagc 1412

cagcggaggg cgctcagtga gtgccccggg ctttctagac aacaggcagg aaggatgaac 1472

ctcagggcac cccaggtgg tgccgaaagc caggcagttg ggacagaggt gcccacgagg 1532

gcagaggccg gtgctaaggg gatggggaag aagggacaag attcccagag aggagaggag 1592

gctgttggtg ggaaagtggc agggctgggg gagaccacgc cccaagggtc cggggcggag 1652

gatgctttgt tcttttctgg ttttggttcc tctttcgagg ggggtggggg aggtcaacag 1712

ggactgagtg gggcagaggc ccagaagtgc cagcctgggg agccgttttg gggcagcccc 1772

ttctgccac cccatccttc ttctctcca gagatgccag gggggcgtgt atgctctgcc 1832

ccttcctca gacaggggct ggggtggggag gctctttagg ctcaggagaa gcattttaaa 1892

gaaaccccca cctgcccgc cgcattataa acacaggaga ataataata gaataaaagt 1952

gaccgactgt caaaaaaaaa aaa 1975

<210> 2
<211> 353
<212> PRT
<213> Homo sapiens

<400> 2

Met Ser Lys Pro Pro Asp Leu Leu Leu Arg Leu Leu Arg Gly Ala Pro
1 5 10 15

Arg Gln Arg Val Cys Thr Leu Phe Ile Ile Gly Phe Lys Phe Thr Phe
20 25 30

Phe Val Ser Ile Met Ile Tyr Trp His Val Val Gly Glu Pro Lys Glu
35 40 45

Lys Gly Gln Leu Tyr Asn Leu Pro Ala Glu Ile Pro Cys Pro Thr Leu
50 55 60

Thr Pro Pro Thr Pro Pro Ser His Gly Pro Thr Pro Gly Asn Ile Phe
65 70 75 80

Phe Leu Glu Thr Ser Asp Arg Thr Asn Pro Asn Phe Leu Phe Met Cys
85 90 95

Ser Val Glu Ser Ala Ala Arg Thr His Pro Glu Ser His Val Leu Val
100 105 110

Leu Met Lys Gly Leu Pro Gly Gly Asn Ala Ser Leu Pro Arg His Leu
115 120 125

Gly Ile Ser Leu Leu Ser Cys Phe Pro Asn Val Gln Met Leu Pro Leu
130 135 140

Asp Leu Arg Glu Leu Phe Arg Asp Thr Pro Leu Ala Asp Trp Tyr Ala
145 150 155 160

Ala Val Gln Gly Arg Trp Glu Pro Tyr Leu Leu Pro Val Leu Ser Asp
165 170 175

Ala Ser Arg Ile Ala Leu Met Trp Lys Phe Gly Gly Ile Tyr Leu Asp
180 185 190

Thr Asp Phe Ile Val Leu Lys Asn Leu Arg Asn Leu Thr Asn Val Leu
195 200 205

Gly Thr Gln Ser Arg Tyr Val Leu Asn Gly Ala Phe Leu Ala Phe Glu
210 215 220

Arg Arg His Glu Phe Met Ala Leu Cys Met Arg Asp Phe Val Asp His
225 230 235 240

Tyr Asn Gly Trp Ile Trp Gly His Gln Gly Pro Gln Leu Leu Thr Arg
245 250 255

Val Phe Lys Lys Trp Cys Ser Ile Arg Ser Leu Ala Glu Ser Arg Ala
260 265 270

Cys Arg Gly Val Thr Thr Leu Pro Pro Glu Ala Phe Tyr Pro Ile Pro
275 280 285

Trp Gln Asp Trp Lys Lys Tyr Phe Glu Asp Ile Asn Pro Glu Glu Leu
290 295 300

Pro Arg Leu Leu Ser Ala Thr Tyr Ala Val His Val Trp Asn Lys Lys
305 310 315 320

Ser Gln Gly Thr Arg Phe Glu Ala Thr Ser Arg Ala Leu Leu Ala Gln
325 330 335

Leu His Ala Arg Tyr Cys Pro Thr Thr His Glu Ala Met Lys Met Tyr
340 345 350

Leu

a'
ord.